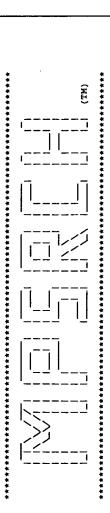
US-08-912-951-1.rge



Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

IIPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Mon Aug 3 13:21:28 1998; MasPar time 5366.00 Seconds 1374.553 Million cell updates/sec Run on:

oular output not generated.

>US-08-912-951-1 (1-4015) from US08912951.seq 4015

Title: Description: Perfect Score: N.A. Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 Nmatch STD

532261 seqs, 918536377 bases x Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

embl55 1:em_ba 2:em_htg 3:em_huml 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro genbank107 Database:

12:9b_ba 13:9b_htg 14:9b_in 15:9b_om 16:9b_ov 17:9b_pat 18:9b_ph 19:9b_pl 20:9b_pr1 21:9b_pr2 22:9b_ro 23:9b_st 24:9b_sts 25:9b_sy 26:9b_un 27:9b_v1 Mean 12.056; Variance 6.037; scale 1.997 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No. Score Query No. Score Match Length DB ID Description 1 4015 100.0 4015 21 AF015950 Homo sapiens telomeras 2 4001 99.7 4027 21 AF018167 Homo sapiens telomeras 3 43.9 85.7 8960 22 AF043739 Synthetic construct hu 920 22.9 3426 22 AF043739 Synthetic construct hu 920 22.9 3426 22 AF043739 Synthetic construct hu 49 1.2 201 22 AF029235 Mus musculus telomeras 67 1.2 218 17 166494 Sequence 14 from patent 10 36 0.9 215 17 128278 Sequence 14 from patent 10 36 0.9 215 17 128278 Sequence 5 from patent 10 36 0.9 255 17 128278 Squence 5 from patent 10 36 0.9 201 17 A10161 Synthetic DNA for prep 12 30 0.7 201 17 A10162 Synthetic DNA for prep 13 30 0.7 201 17 A10159 Synthetic DNA for prep 13 30 0.7 201 17 A10159 Synthetic DNA for prep 14 30 0.7 201 17 A10159 Synthetic DNA for prep 215 216 216 217 201 2	Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	2.00e-73	3.56e-26	1.15e-13	4.08e-09	5.00e-06	1.98e-05	5.17e-02	5.17e-02	5.17e-02	5.17e-02	5.96e-01
Score Match Length DB Match DB	Description	Homo sapiens telomeras	Homo sapiens telomeras	Synthetic construct hu	Mus musculus telomeras	Mus musculus telomeras	14	14			gDNA encoding envelope	Synthetic DNA for prep	S.griseus gene for pre	Synthetic DNA for prep	S.griseus gene for pre	gDNA encoding envelope
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SCORE 4015 4015 4015 920 129 67 67 67 67 83 30 30 30 30 30	Length	4015	4027	8960	3426	201	7218	7218	215	215	565	201	201	201	201	565
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DEFINITION	HOHO		sapiens	tel	telomerase	ase reverse		transcriptase (hTRT) mR	mRNA, complete
ACCESSION	AF01	5950							
NID	q2330016	0016							
KEYWORDS									
SOURCE	human								
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Gaddle,S.D., Ziaugra,L., Beljersbergen,R.L., Davidoff,M.J., Liu,Q.,
Bacchetti,S., Haber,D.A. and Welnberg,R.A.
hEST2, the putative human telomerase catalytic subunit gene, is
up-regulated in tumor cells and during immortalization
Gell 90 (4), 785-795 (1997)
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Meyerson,M., Counter,C.M., Eaton,E.N., Ellisen,L.W., Steiner,P.,
Caddle,S.D., Zlaugra,L., Beljersbergen,R.L., Davidoff,M.J., Liu,Q.,
Bacchetti,S., Haber,D.A. and Weinberg,R.A.
Direct Submission
Submitted (11-AUG-1997) Whitehead Institute for Biomedical
Research, Massachusetts Institute of Technology, Nine Cambridge
Center, Cambridge, MA 02142, USA
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LLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV
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GGTARYOMPAHGLEPWGLLLDTRTLEYQSDYSSYATSIRASLTRNGFRAGRNMRR
KLFGVLRLCHSLFLDLQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQOVWKNPT
FFLRVISDTASLCYSILKAKNAGMSLGARGAGPLPSEAVQWLCHQAFLLKLTRHRVT
YVPLLGSLRTAQTQLSKLLPGTTLTALEAAANPALPSDFKTILD*
1361 c 1277 g 715 t
                                                      AF018167 4027 bp mRNA PRI 29-AUG-1997
Homo sapiens telomerase catalytic subunit (hEST2) mRNA, complete
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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/note="member of reverse transcriptase class"
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Length 4027 Indels

Score 4001; DB 21; Pred. No. 0.00e+00; 0; Mismatches 2;

Query Match 99.7%; Best Local Similarity 100.0%; Matches 4003; Conservative

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                                     GTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGCGATGCCGCGCGCTCCC
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GIGGAGACCAIC	CGCCTGCCCCAG	GCGCAGTGCCCC 	CCAGCAGCCGGT	GAGGACACAGAC	GTGTACGGCTTC 	AGGCACAACGAA 	GCCAAGCTCTCG	CGCAGGAGCCCA	CTGGCCAAGTTC	TTTTATGTCACG	TGGAGCAAGTTG	CTGTCGGAAGCA 	CTCCGCTTCATC	GGAGCCAGAACG GGAGCCAGAACG	CIGITCAGCGIG 	CTGGGCCTGGAC 	GACCGCCGCCTI 	CCCCAGGACAGG
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	CCAGGGACTCCC CAGGGACTCCC	TTTCTGGAGCTG 	TGCCCGCTGCGA 	36CTCTGTGGCG	GCCAGCACAGC	STGCCCCAGGC 	AAGTTCATCTCC	AGCGTGCGGGGC	SAGCACCGTCTG	STCGTCGAGCTG	CTCTTTTCTAC	TTGAAGAGGGTG 	AGGCCGCCCTG	ATTGTGAACATG 	CGTCTCACCTCG	11111111111111111111111111111111111111	TTCGTGCTGCGT 	STGACGGGCGCG
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CTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCAGGACAGGCTC 2230 TATTCCCTGGTGCGGCCTGCTGGTGGATACCCGGACCCTGGAGGTGCAGCGACGTGCAGCGACTGCAGCGACGTGCAGCGACCTGGAGGTGCAGCGACCTGGAGGTGCAGGTGCAGCGACCTGGAGGTGCAGGCGAC TGGATTTGCAGGTGAACAGCCTCCAGACGGTGTCCACCAACATCTACAAGATCCTC AGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCG GGATGCCGTCGTCATCGAGCAGAGCTCCTCCTGAATGAGGCCAGCAGTGGCCTC ACGRICTICCTACGCTTCATGTGCCACCACGCGTGCGCCATCAGGGGCAAGTCCTAC GAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTG GAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCGCCGCCGCCCTCTG GCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTT CGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACAC CCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACC NGAACCCCACATITITICCTGCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCC

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Telomerase activity is restored in human cells by ectopic expression of hTERT (hEST2), the catalytic subunit of telomerase Oncogene 16 (9), 1217-1222 (1998)
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                                                                    CGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGG
                                                                                                                                                                CGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAGACGCTGAGTCGG
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                                                                                                          GACTTCAAGACCATCCTGGACTGATGGCCACCCCCCACAGCCAGGCCGAGAGCAGCAC
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FLELLGHRAQCPYGTULKTHCPLRAAYTPAGGYCARREPOGSYAAPEEDTDFRLLY
ILRQHSSPWQYYGFVRACLRRLYPPGLWGSRHNERRELRNTKKFISLGKHAKLSLQEL
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TFQKRUELFYRKSYWSTLGSGIGTHGHRANGTRFHYDHMSYYVELLRSFRYTYTET
TFQKRUELFYRKSYWSTLGSGIGTHGKLRWQLRELSSAEVRQHREARPALLTSKLRF
DENDGIRLFYRMSYWGARTFRRERARLSFSRYALFSYLMYERARPALLTSKLRF
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NEASSGLEDVLLRLYNDHTHAKTFLRTLYRGYPAHLCGETSPLRADAYUEQSSSL
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GGTAFVQMPAHGLFFWCGLLLDTRTLEVQSDYSSTARTSIRASLTFNRGFRAGRNMRR
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LLDGARGGPPEAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDVLVHLLARCALFV
LVAPSCAYQVCGPPLYQLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPA
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RPAEEATSLEGALSGTRHSHPSVGRQHHAGPPSTSRPPRPWDTPCPPVYAETKHFLYS
SGDKEQLRPSFLLSSLRPSLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPL
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FFLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSEAVQWICHQAFLLKLTRHRVT
YVPLLGSLRTAQTQLSRKLPGTTLTALEAAANPALPSDFKTILDYPYDVPDYAGYPYD
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/db_xref="PID:93023055"
/translation="MPRAPRCRAVRSLIRSHYREVLPLATFVRRLGPQGWRLVQRGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1101 CGICCIGCIGCGCACGIGGGAAGCCCIGGCCCCGGCCACCCCGCGAIGCCGCGCGCTCC 1160
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                                                                                                                                                                                                                                                                            /organism="Cloning vector pCI-neo"
/db_xref="taxon:45772"
1102. .4542
/note="telomerase catalytic subunit hTERT/hEST2 mRNA"
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 cacerroerecececroececcocaecerecececroerecaecececececece 189
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/note="engineered based on the epitope for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="hTERT/hEST2"
1147. 4605
10te="telomerase/reverse transcriptase"
/codon_start=1
                                                                                                                                             db_xref="taxon:32630"
order(1. 1101,4606. 8960)
/note="mammalian expression vector;
Number 047120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3439; DB 25;
Pred. No. 0.00e+00;
0; Mismatches 2;
                                                                                                              /organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2038 t
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2551 c 2484 g 2
Location/Qualifiers
1. .8960
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                 Cambridge, MA 02142,
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Best Local Similarity 99.9%;
Matches 3441; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="5p15.
1102. .4542
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CTITCCGCGCGCTGGTGCCTGGTGTGCGTGCCCTGGGACGCACGGCCGCC 249	CCGCCGCCCCTCCTTCCGCCAGGTGTCCTGCCTGAGGAGCTGGTGGCCCGAGTGCT 1400 	CAGAGGCTGTGCGAGCGCGGCGAAGAACGTGCTGGCCTTCGGCTTCGCGCTGCTGGA 1460 	GGGCCCCCGGGGGCCCCCCCGAGGCCTTCACCACCGGGGCCCACCTACCT	CACGGTGACCGACGCACTGCGGGGGGGGGGGGGGGCTGCTGTTGCGCCGCGTGGG 1580 	GACGACGTGCTGGTTCACCTGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAG 1640 	CTGCGCCTACCAGGTGCGGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCG 1700 	CCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCA 1760 	AGGGTCAGGGAGGCCGGGGTCCCCTGGGCTGCCAGCCCCGGGTGCGAGGCGCGG 1820 	GGCAGTGCCAGCCGAAGTCTGCCCGTTGCCCAAGAGGCCCAGGCGTGGCGCTGCCCCTGA 1880 	CCGGAGCGGACGCCCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACC 1940 	GTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCGCCGAAGAAGCCACCTCTTT 2000 	GGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCATGGGCCGCCAGCACCACCACCACCACGC 2060 	GCCCCCCATCCACATGGGGGCCACCACGTCCCTGGGACAGGCCTTGTCCCCCGGTGTA 2120 	GCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCGGCTGCGGCCCTCCTT 2180 	CTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCCCGGAGGCTCGTGGAGACCATCTT 2240 	CTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCCGCCTGCCCAGCG 2300 	CTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTA 2360 	GGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCCCCCAGCCGGTGT 2420
190 GG	1341 CC 	1401 GC 11 310 GC	1461 CG 11 370 CG	1521 CA 11 430 CA	1581 CG 11 490 CG	1641 CT 550 CT	1701 GC 610 GC	1761 TA 670 TA	1821 GG 1 730 GG	1881 GC 	1941 GAG' 850 GAG'	2001 GG 910 GG	2061 GGG(970 GGG(2121 CG 1030 CG	2181 CC 1090 CC	2241 TC 1150 TC	2301 CT 1210 CT	2361 CC
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3140 2780 2840 2900 2960 3080 2049 3200 3440 2480 2540 2660 1629 1689 1690 GCACTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGTCTTTTTTTATGTCACGGA 1749 1809 3020 1989 2109 3260 2169 3320 2229 3380 2409 1510 CCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCT 1570 GCAGGAGCTGACGTGGAAGATGAGCGTGCGGACTGCGCTTGGCTGCGCAGGAGCCCAGG 1630 GGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCT 2841 GACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGTAGTTGCA 1750 GACCACGTTTCAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCA 1810 AAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTGGAAGCAGA 3201 TATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCCTGA 2290 CGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTTAC GGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCT AAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGA 2110 TATCCACAGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCCAGGACCCGCCGCCTGA CTGTGCCCGGGGGGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCC GCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTGCGCAGGAGCCCAGG CGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTAC CCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTCGCT 2721 3441 2350 2541 2661 2901 3381 2421 2601 . _ ^ 0 _

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KITRIJAQCIVCMHWGSQPPADLSFHQVSSIKELVARVVQRLCERNERNVLARGFE
LLNRERGGPBMAFTSSVRSYLDNTVIETLRYSGAWHLLLSRYGDDLLYYLLAHCALYL
LLYPPSCAYQVGSPLYQICATTDIWBSVSASYRPTRYGRNFTNLRFLQQIKSSSRQE
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ARSPEVPTAEKDLSSKGKVSDLSLSGSVCCKKKPSSTSLLSPPRQNAFQLRPFIETRH
FLYSRGDGGERLNPSFLLSNLQPNLTGARRLYBIJFLGSRRYSP
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VYGFLAACLCKTVVSASLMGTRHNERRFFKNIKKFISLGKTGRISLOELMWKKNYEDCH
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FDFFLHFLRHSVVY GRORYTVGCGIPQGSSLSTLLCSLCFGDMERKLFAEVORDGIL
LRFVDDFLLVTPHLDQAKTFLSTLVHGVPEYGCMINLCKTVVNFPVEFGTLGGAAPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
product=ttelomerase reverse transcriptase"
/db_xref="PID:93005592"
/translation="WIRAPRCPAVRSLIRSRYREWWDLATFVRRLGPEGRRLVQPGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKCHGLFLDLQVNSLQTVCINIYRIFLLQAYRFHACVIQLFFDQRVRKNLTFFLGIIS
SQSSCCYALIKVKNPGMTLRAGGSFPFBAAHMLCYQAFLLKLAAHSVIYKCLLGFLRT
AQKLLCKRLPEATWTINSTAFPFBABAFFLDFQTILD"
979 c 907 g 794 t
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3426)

1 (bases 1 to 3426)

Expression of mouse telomerase reverse transcriptase during development, differentiation, and proliferation on coogene (1998) In press (bases 1 to 3426)

2 (bases 1 to 3426)

Greenberg, R.A., Allsopp, R.C., Chin, L., Morin, G.B. and DePinho, R.A. Direct Submission of Microbiology and Immunology, Albert Submitted (02-MAR-1998) Microbiology and Immunology, Albert Enstein College of Medicine, 1300 Morris Park Ave., Bronx, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                        cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .3426
Action/Coganism="Mus musculus"
Ab_xref="taxon:10090"
Achromosome="13"
Achromoso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
02-APR-1998
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3426 bp mRNA ROD 02-APR-1998 telomerase reverse transcriptase mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 CAGCCGATACCGGGAGGTGTGGCCGCTGGCAACCTTTGTGCGGCGCCTGGGGGCCCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 CAGCCACTACCGCGGGGGGGCGCCGCGGCGCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 CIGGGGGTGGTGCAGCGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 CAGGCGGCTTGTGCAACCCGGGGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80;
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Pred. No. 0.00e+00;
0; Mismatches 979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="mTERT"
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Best Local Similarity 69.2%;
Matches 2379; Conservative
                                                   musculus
                                                                                                                                                                                                                                                                                                           musculus
                                                                                                                                                                                                                                                             house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10461, USA
                                                                                       AF051911
g3005591
AF051911
Mus muscu
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1046 1032 1092 1103 1152 1163 1212 1223 1263 1283 1299 1343 912 932 972 339 399 433 459 553 579 613 639 673 969 733 756 793 852 TGCATGGATGCTACTGTTGAGCCGAGTGGGCGACGACCTGCTGGTCTACCTGCTGGCACA 493 ----G-ACT----C-CT-C-AG-----GTCACATT-GCAG---GTTTC---GAACAGCA-A AGACGCACTGCCCCCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTGTGCCCGGGAGA GTACCAAATTTGTGCCACCACGGATATCTGGCCCTCTGTGTCCGCTAGTTACAGGCCCAC CCGACCCGTGGGCAGGATTTCACTAACCTTAGGTTCTTACAACAGATCAAGAGCAGTAG TCGCCAGGAAGCACCGAAACCCCTGGCCTTGCCATCTCGAGGTACAAAGAGGCATCTGAG GGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTT GCCCAAGAGGCCCAGGCGTGCCCTGAGCCGGAGCGGACGCCCGTTGGGC-AGG GGAGGAGGGACCCCACAGGCAGGTGCTACCAACCCCATCAG-GCAAATCATGGGTGCCAA GTCCTGCTCGGTCCCCCGAGGTGCCTACTGCAGAGAAAGATTTGTCTTCTAAAGGAAAGG CACCTGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCG-CT-CTCT-GGCACGC TGTCTGACCTGAGTCTCTCTGGGTGTGCTGTAAACACAAGCCCAGCTCCACATCTC -GCCACTCCCACCCATCCGTGGGCCGCCA-GCACCACGCGGGCCCCCCA-TCCACATCGC TGCTGTCACCACCCCGCCAAAATGCCTTTCAGCTCAGGCCATTTATTGAGACCAGACATT GCCCACCACGTCCCTGGGACAC-GCCTTGTCCCCC-GGTG-TACGCCGAGACCAAGCACT TCCTTTACTCCAGGGGAGATGGCCAAGAGCGTCTAAACCCCTCATTCCTACTCAGCAACC TCCAGCCTAACTTGACTGGGGCCAGGAGACTGGTGGAGATCATCTTTCTGGGCTCAAGGC CTAGGACATCAGGACCACTCTGCAGGACACCCGTCTATCGCGTCGATACTGGCAGATGC CCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGC CTGTGCTCTTTATCTTCTGGTGCCCCCCAGCTGTGCCTACCAGGTGTGGGGTCTCCCCT GTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACGCTAGTGGACCCCGAAG GCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTC--AGGG-AGGCCGGGGTCCCCCT ATCCCTGAAAGAGCTGGTGGCCAGGGTTGTGCAGAGACTCTGCGAGGGCGCAACGAGAAA CGTGCTGGCTTTTGGCTTTGAGCTGCTTAACGAGGCCAGAGGCGGGCCTCCCATGGCCTT CACTAGTAGCGTGCGTAGCTACTTGCCCAACACTGTTATTGAGACCCTGCGTGTCAGTGG TCTCACCAGTACAAGTGTGCCTTCAGCTAAGAAGGCCAGATGCTATCCTGTCCGGAGAGT 254 918 913 1264 1284 280 1033 1093 1153 1164 1213 1224 220 340 434 640 674 697 757 853 933 973 990 1104 314 374 400 460 520 554 580 614 734 794 816 1047 494 ò g 8 ö ద ò ద õ 셤 B ð 8 8 8 8 8 8 පු δ ద ò 요 ð g ç 셤 ò g ò 요 õ 셤 à ç

2187 1587 AGGACACCTGGCTAGCCCATCTGCAGACTGCGCTTCATCCCCAAGGCCCAAGGCC 1887 2067 2307 1407 1644 ceeccecadaccaccercrecercadagarrecreeccaagrrecreecrearga 1703 1648 ACACATACGTGGTACAGCTGCTTAGGTCATTCTTTTACATCACAGAGCCACATTCCAGA 1707 ----TGACAGATGCCTTG-A--AC-AC-CAGCCCACG-CACCTCATGG GCAAGGIGGIGICIGCIAGICICIGGGGIACCAGGCACAAIGAGCGCCGCTICIIIAAGA 1524 ACACCAAGAAGTICATCTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGT CCGCTGCAGAGCACCGTCTGAGGGAGAGGATCCTGGCTACGTTCCTGTTCTGGCTGATGG AGAACAGGCTCTTCTTCTACCGTAAGAGTGTGTGGAGCAAGCTGCAGAGCATTGGAGTCA GGCAACACCTTGAGAGAGTGCGGCTACGGGAGCTGTCACAAGAGGAGGTCAGGCATCACC 1944 TGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAAAAAA AGGCCCAGCATTTCACCCAGCGTCTCAAGACTCTCTTCAGCATGCTCAACTATGAGCGGA 2004 GGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGAGCGGG AGGCAGATGTGACCGGGCCTATGATGCCATCCCCCAGGGTAAGCTGGTGGAGGTTGTTG CCAATATGATCAGGCACTCGGAGGAGCACGTACTGTATCCGCCAGTATGCAGTGGTCCGGA AGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCCACGTCTCTACCTTGACAGACC TCCAGCCATACATGGGCCAGTTCCTTAAGCATCTGCAGGATTCAGATGCCAGTGCACTGA 1344 AGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACACAGACCCCCGTCGCCTGGTGC ATTIGCTCCGCCTGCACAGCAGTCCCTGGCAGGTATATGGTTTTCTTCGGGCCTGTCTCT GGAAGATGAAAGTAGAGATTGCCACTGGCTCCGCAGCAGCCCGGGGAAGGACCGTGTCC CGCGGCGCCCCCGGCCTCTGTGCTGGGCCTGGACGATATCCACAGGGCCT GAGATAGCCAAGGCCAAGTCCATTTAGGAGACAGGTCACCACCCTCTGACC **ACTTAAAGAAGTTCATCTCGTTGGGGAAATACGGCAAGCTATCACTGCAGGAACTGATGT** ACCAACAGG. 1588 1764 1824 1828 1948 1404 1704 1708 1768 1888 2064 2068 2124 2184 2244 2248 1300 1408 1468 1528 2008 2128 2188 2301 2308 1348 g 셤 용 à 셤 ò 셤 å 셤 ò 유 à 셤 à 셤 à g å 용 ò g ò ద ò g ò g ò ò ద ò ò 셤 ò 원

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2595 GCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGG
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                                         2428 ACTICTICCTGCACTICCTGCGTCACAGIGTCGTAAAGAITGGTGACAGGTGCTATACGC
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2 (bases 1 to 201)
Drissi,R. and Cleveland,J.L.
Drissi,R. and Cleveland,J.L.
Drisct Submission
Submitted (07-007-1997) Biochemistry, St jude Children's Research
Hospital, 332 North Lauderdale, Memphis, TN 38105, USA
Location/Qualifiers
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                                                                                                                  Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 201)
Drissl, R. and Cleveland, J.L.
Partial sequence of Mus musculus telomerase catalytic subunit
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                telomerase catalytic subunit mRNA, partial cds
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
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/organism="Mus musculus"
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       Score 67; DB 17; Length 7218;
Pred. No. 3.56e-26;
211; Mismatches 153; Indels
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Dorner,F., Schelflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
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                   Local Similarity
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2629 GCGGGACGGCTGCTCCTCCTTGGTGGATTTTTTTTTGTTGGTGACACCTCAC 2688
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                                                                                                                      30-0CT-1996
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Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use
control fungal disease
Patent: US 5569830-A 5 29-0CT-1996;
Location/Qualifiers
                                                                                                                                                                                                                                                                          1 (bases 1 to 215)
Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H.
Plant inhibitors of fungal polygalacturonases and their use control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
1828 CIGICIGATICCAAIGCTITIGCAACTIGCICCAGACACTICCTGGGTAGAAAA 1776
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Pred. No. 4.08e-09;
82; Mismatches 90; Indels
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Pred. No. 5.00e-06;
64; Mismatches 68; Indels
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Sequence 5 from patent US 5569830.
128278
91819054
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Sequence 5 from patent US 5569830.
128278
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a 8 c 25 g
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Best Local Similarity 15.5%;
Matches 32; Conservative
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Local Similarity 14.2%;
nes 22; Conservative
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Garvin, R.T. and James, E.
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1 (bases I to 563)

1 (bases I to 563)
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                                  110 TDGNRSGADSYGSSKTA-MTSRNRTGKTANNAVDSRNMGDASVGSDKNTKKHAKNSADGK 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 GYRYBCCYTGYGGSGARRRYRRYNNYTCBMGNTGYTGGGYRGCGCTBACYCCCACGS 292
                                                                                                                                                                                                                                                                                                    E04076 565 bp RNA PAT 26-NOV-1996
gDNA encoding envelope region of type C hepatitis virus.
E04076
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Synthetic DNA for preproprotease leader & prochymosin.
A10161
9490655
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Pred. No. 1.98e-05;
58; Mismatches 66; Indels
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strandedness: Single;
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/organism="Hepatitis C virus"
/db_xref="taxon:11103"
1 93 c 107 g 85 t
                                                                                                                                                                                          1008 TCCCAGGGACGTGGTGGGATGTGGGT 974
                                                                                                                                                  169 VGSKNNGDRNNRYGTGTKSNVSNNCGGGNKRDVSS 203
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Location/Qualifiers
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JP 1992349885-A/1
04-DEC-1992
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Best Local Similarity 31.7%;
Matches 59; Conservative
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unclassified.
1 (bases 1 to 201)
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Hepatitis C virus.
Hepatitis C virus
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PN JP 199234988
PD 04-DEC-1991
PF 29-MAY-1991
PI MORINAGA TSU
ICHIKAWA YATARO
PC C12N15/10,C10
CC strandedness
CC topology: Li
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/product-"preproprotease leader & prochymosin"
Ab_xxef-"piD:9490656"
Aranslation-"HHSPVSPAESPAPQPGRPRPVSRRLLEGGAAVLGALALSASP
LTAQAAVRRAAREITRIPLYKGK"
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| Abs.xref-"prig49(1977
| /translation-"MHSPVSPAESPAPQPGRPRPVVSRRLLEGGAAVLGALALSASP
| LTAQAAVRRAAADEPPBWNDFGV"
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Production of active proteins containing cystine residues Patent: EP 0222279-A 5 20-MAY-1987; Cangene Corporation
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1 (bases 1 to 201)

2 (astron. T. and James.E.

Production of active proteins containing cystine residues
Patent: EP 022279-A 2 20-MAY-1987;
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35; Mismatches 57; Indels
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35; Mismatches 57; Indels
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S.griseus gene for preproprotease (partial).
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/organism="Artificial sequences"
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Matches 52; Conservative
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1 (bases 1 to 201)
Garvin,R.T. and James,E.
Production of active proteins containing cystine residues
Patent: EP 0122279-A 6 20-MAY-1987;
Cangene Corporation
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Eubacteria; Firmicutes; Actinomycetes; Streptomycetes;
Streptomycetaceae; Streptomyces.
1 (bases 1 to 201)
Garvin, R.T. and James, E.
Production of active proteins containing cystine residues
Patent: EP 0222279-A 3 20-MAY-1987;
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Synthetic DNA for preproprotease leader & prochymosin.
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/organism="Streptomyces griseus"
/db_xref="taxon:1911"
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/organism="synthetic cc
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JP 1992349885-A/1.
Hepatitis C virus.
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepatitis C-11ke viruses.
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NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
NUCLEIC ACID FRAGMENT WITHIN ENVELOPE REGION OF HEPATITIS C VIRUS
PATENT: JP 1992349885-A 1 04-DEC-1992;
TEIJIN LTD
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117 CSAGSAGSCGSCGSGASACSACSGGSCGSGGSCGSCCSGGCTGSGGSGCSGGSGACTCSG 176
                      E04076 565 bp RNA PAT 26-NOV-1996 9DNA encoding envelope region of type C hepatitis virus. E04076
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JP 192349885-A/1
04-DEC-1992
29-MAY-1991 JP 1991152169
MORINAGA ISUTAE, CHAYAMA KAZUAKI, KUMADA HIROMITSU, PI
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Pred. No. 5.96e-01;
54; Mismatches 56; Indels
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/organism="Hepatitis C virus"
/db_xref="taxon:11103"
a 93 c 107 g 85 t
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Job time : 10668 secs.
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Location/Qualifiers
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                                                                                                                          Query Match 0.7%;
Best Local Similarity 22.9%;
Matches 33; Conservative
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PN JP 199234988
PD 04-DEC-1992
PF 29-MAY-1991
PI MORINAGA TSU
ICHIKAWA YATARO
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MasPar time 631.45 Seconds 865.070 Million cell updates/sec n.a. • n.a. database search, using Smith-Waterman algorithm Mon Aug 3 16:19:35 1998; MPsrch_nn .. 0 Run

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Title:

>US-08-912-951-1 (1-4015) from US08912951.seq 4015 Description: Perfect Score: N.A. Sequence: Sequence: Comp:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch 188442 seqs, 68026449 bases x Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

n-geneseq32 Database:

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Variance 6.348; scale 1.587 Mean 10.074; istics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Oligonucleotide probe	Oligonucleotide probe	Human endothelin-1 an	Base substituted E.co	Human neutrophil elas	Generic DNA sequence	Generic DNA sequence	Human interleukin 8 a	Human interleukin 8 a	Base substituted E.co	Substance P receptor	Generic DNA sequence	Generic DNA sequence
SOMMANTES	A	Q51746	051746	T76405	N81164	T76274	070466	070469	T76363	T76363	N81164	T76445	070465	070468
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Gaps Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
(Q51735). It hybridized to all spp. of mycobacteria tested, but
cross reacted to a few non-mycobacterial spp. The probe may
be useful as an initial screen for mycobacterial infection.
See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T; 6 cggcgssvhsyyvvhvvshhhsvhhvvhvhvsvvvvhhvvhvvhhvhyhvyvsv 60 31-MAY-1994 (first entry) Oligonucleotide probe MK14-A Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; Shank DD, Spears PA; WPI; 93-378844/48. New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in 1.1%; Score 45; DB 9; Length 91; Similarity 7.3%; Pred. No. 2.21e-10; 4; Conservative 46; Mismatches 5; Indels EP-571911-A. 01-DEC-1993. 24-MAY-1993; 108325. 26-MAY-1992; US-889651. (BECT) BECTON DICKINSON CO. Shank DD. Spears PA; Query Match Best Local Similarity Synthetic. sambles Matches 셤 ö

LT 2 Q51746 standard; cDNA; 91 BP RESULT ID Q5

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COSTACTOR

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WO9640162-A1.
                                                                                                                                                                                                                                         misc_feature
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Solum 5: Page 38: 71pp; English.

Claim 5: Page 38: 71pp; English.

C A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine content of the involves the topical administration of an essentially adenosine free antisense oligonuclectide specific content be present sequence is an antisense oligonuclectide specific for the human endothelin-1, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, cc asthma, chronic obstructive pulmonary diseases, bronchitis and other airway diseases characterised by an inflammatory response. By climinating adenosine from the antisense on, its liberation upon cc antisense degradation is prevented, thereby preventing adenosine-constitution in patients with hyper-reactive airways.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCACCCCCCGCGATGCCGCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 tccggcgssvhsyyvvhvvshhhsvhhvvhhvhvvhhvvhhvhyhvyvsvct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                      EP-571911-A.
24-MAY-1993.
24-MAY-1993, 108325.
26-MAY-1992; US-889651.
26-MAY-1992; DECTON DICKINSON CO.
Shank DD, Spears PA;
WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria - used for detection and amplification of Mycobacteria nucleic acid in
                                                                                                                                                                                                                                                                                                               Oligonucleotide probe MK14.A consists of nucleotides 5-95 of 1 (Q51735). It hybridized to all spp. of mycobacteria tested, lcross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q1735.45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
             31-MAY-1994 (first entry)
Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-SEP-1997 (first entry)
Human endothbelin-1 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db >,
2.21e-10;
'-haq 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB 9;
Pred. No. 2.21e-
45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of airway diseases such as
                                                                                                                                                                                                                                                                                               Claim 3; Page 14; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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T76405 standard; DNA; 178 BP.
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larity 37.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 1.1%;
Local Similarity 11.9%;
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-DEC-1996.
06-JUN-1996; U09306.
07-JUN-1995; US-474497.
(UYEC-) UNIV BAST CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metzger WJ, Nyce JW;
WPI; 97-051871/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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PR (SUSO) SUOMEN SOKERI OY.

PA (SUSO) SUOMEN SOKERI OY.

PI Lehtcovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;

DR WP1: 88-279927/40.

PT Introducing random point mutations into nucleic acods -

Introducing random point mutations into nucleic acods -

PT misincorporation, completion of molecules and screening.

PT misincorporation, while type sequence was obtained as a bisclosure; p; English.

CC Random point mutations were introduced into the alpha fragment of CC E.coll beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonuclectide was hybridised to it to generate a popn of DNA molecules which terminate at all CC possible nucleotide postitions within a specified region. The cariable 3' ends generated in this way are used as primers for reverse transcriptase and the molecules are misincorporated by the CC reverse transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

CT he sequence covers all 176 difft base substitutions, most of which sequence and the may given mutant.

Secuence of the sequence of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 thhyrrmrbnvyrdynrsdaaawyccyrrsvkydccynachhddh-yvybbbvynvhnhn 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elongation,
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06-JUN-1996, U03-474497.
(UYEC-) UNIV EAST CAROLINA.
Metzger WJ. Nyce JW;
WPI: 97-051871/05.
Treatment of alrway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
W81164 standard; DNA; 204 BP.
N81164;
N8 NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; ss.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neutrophil elastase (medullasin) antisense oligonucleotide. Asthma; airway epithelium; adenosine free; cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 Others;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45; DB 1; Length 204;
Pred. No. 2.21e-10;
54; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/function=multiple cloning site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3176 TCCCTCTGCTACTCCTGAAAGCCAAGAACGCA 3211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 ncncccbnnhvchnvhbnnhrnwayvrhdarrddvh 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualiflers
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T76274 standard; DNA; 317 BP.
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|larity 12.5%;
|Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T76274;
15-SEP-1997 (first entry)
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les 12; Conser
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070469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A method for treating alrays disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonuclectide (ON) to the airway epithalium of the subject. The present sequence is an antisense oligonuclectide specific for the human neutrophil elastase (medullasin), targeted at the finitation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine induced bronchoconstriction in patients with hyper-reactive airways. Sequence 317 BP; O A; 112 C; 118 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain bisclosure; Page 35; 255pp. English.

070466 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides This generic formula can also be represented as follows:X(NMB)1(TGC) (NNB)10(TGC)2(NNB)4Z(NNB)8(TGC)(NNB)-9Y. X and Y are flanking restriction sites (X is not the same as Y)
                                                                                                                                                                                                                                                                      95 ttgggc-gcbbtcbgggtg-gcgccgcbgbbgtggcctccgcgcbcbgggbcbccb 152
                                                                                                                                                                                                                                                                                                                       ACGCACGCCCCCCCCCCCCCCCCTCCCAGGGTGTCCTGCAAAGAG-CTG 295
                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generic DNA sequence to generate a random TSAR-9 petide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                             5; Gaps
                                                                                                                                                                                                                                                    35 beebeeegebeegeggbegtttbebttegeebegebgtgegggeegbebtgbegbbg
                                                                                                                                                                                                                                                                                                                                                                                                                212 gtgccccccbgcbggccggcbggbcbcbggcgbggbgbcbcgcgbgtcggccg
                                                                                                                                                                                                                                                                                                                                                             153 tgbbgggccbcgcgtgggccgcgctc-gccggcccccbcbbtctccgbggccbgcgcg
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                                                                                                                                                                                                   Length 317;
                                                                                                                                                                                                   Score 44; DB 32; Length 317
Pred. No. 7.74e-10;
44; Mismatches 92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 bgggtcbtggtggggctggggct 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 33; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .r 6
070466 standard; DNA; 114 BP.
070466;
05-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
WPI; 94-279739/34.
                                                                                                                                                                                                   Query Match 1.1%;
Best Local Similarity 46.4%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comments)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
subject
Claim 5; 1
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                                                                                                                                                                                                                                                                              28
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ID O7
AC O7
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that are not specified further. Other generic sequences are shown in 070466-68. Other specific peptides generated by these generic sequences are shown in R65151-54. TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The Oilgonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues confer some degree of conformational rigidity to the peptides. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal cuto, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production.

The TSARs are easily characterised and have designed activity allowing directive and therefore activity allowing attents are and accomplex for the conformation or in vivo antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Teomits universe univ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapld; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "this sequence represents '2'; Z can be sequence of 6,9 or 12 nucleotides (see comments)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 bnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.09e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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Q70469 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
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30-DEC-1993; U
31-JAN-1994; U
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subject
Claim 5: Page 36; 71pp; English.
Claim 6: Page 36; 71pp; English.
Claim 6: Page 36; 71pp; English.
Claim 7: Page 36; 71pp; English.
Claim 8: Page 36; 71pp; English.
Claim 9: Page 36; 71pp; English.
Claim 9: Page 36; 71pp; English.
Claim 10: Page 36; 71pp; English.
Claim 10: Page 36; 71pp; Page 31pp; Page 
contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising at TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bgbtgtgcttbccttcbcbcbgbgctgcbgbbbtcbggbggctgccbbgbgpccbcgg 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 TGCGGCGCCTGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGGACCCGGCGGCTTTCC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnnnnn 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 bbgbbtbgctttgctbtctbbggbtcbcbtttbgbcbtbggbbbbcgctgtbggtcbgbb 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 GCGCGCTGGTGCCCAGTGCCTGGTGCGTGCCCTGGGACGCACGGCCGC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-SEP-1997 (first entry)
Human interlicukin 8 antisense oligonucleotide.
Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3.67e-07;
32; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 32;
Pred. No. 3.20e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection in a screening process. Sequence 114 BP; 0 A; 4 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGCACGGCCGCCCCCCGCCCC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T 8
T76363 standard; DNA; 172 BP.
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07-JUN-1995; US-474497.
(UYEC-) UUIV BAST CAROLINA.
Metzger WJ, Nyce JW;
WPI; 97-051871/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7.2%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 32.2%;
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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10 DD 110
110 D
    88888888888888
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human interleukin 8, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense ON, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 172 BP; O A; 35 C; 42 G; 39 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:| | :|:::|: || :| || :| || :| || 3475 CTGGCTGTGGGCCAGTGCCGG 3416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3535 CCCCTCCCTCCCTGGGACGTAGAGCCCGGCGTGACAGGGCTGCTGGTGTCTGCTCTCGGC 3476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 gtbggtcbgbbbgbtgtgcttbccttcbcbcbgbgctgcbgbbbtcbggbbggctgccbb 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Introducing random point mutations into nucleic acods - by prepn of single stranded template, annealing a primer, elongation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 becabbgeateabgabtagetttgetatetabaggateacatttagaeatbaggabbaget 70
                                                                                                                                                                                                                                                                            Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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08-NoV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment.
E.coli beta galactosidase alpha-fragment; base substitutions;
Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SUSO) SUOMEN SOKERI OY.
Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen T;
WPI; 88-279927/40.
                                                                                      Asthma; airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 32; Length 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.09e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 gbgbgccbcggccbgcttggbgtcbtgtttbcbcbcbg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function=multiple cloning site
                                                 15-SEP-1997 (first entry)
Human interleukin 8 antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 36; 71pp; English
                 standard; DNA; 172 BP
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N81164 standard; DNA; 204 BP
                                                                                                                                                             19-DEC-1996.
06-JUN-1996; U09306.
07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CAROLINA.
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Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.0%;
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03-APR-1987;
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                                                                                                                                                                                                                                          Metzger WJ,
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Presenting a recombinant vector library expressing fusion proteins

PT Gentifying proteins or peptide(s) which bind a ligand - by

Screening a recombinant vector library expressing fusion proteins

PT comprising a blanding domain and an effector domain

Disclosure; Page 35; 255pp; English.

CO 70465 is a generic DNA sequence used to generate random TSAR (Totally

CO 70465 is a generic DNA sequence used to generate formula can also be

crepresented as follows: X(NNB) 6(TGC) (NNB) 11Z(NNB) 14(TGC) (NNB) 3Y. X

CC and Y are flanking restriction Sites (X is not the same as Y) that are

CC other specified further. Other generic sequences are shown in Q70466-68.

CC other specified further of the generic sequences are shown in CR 65131-54. TSARs are concatenated by these generic sequences are shown in

CC offility for a ligand and a second effector peptide portion that is

CC affility for a ligand and a second effector peptide portion that is

CC chat the expressed peptide contains 2 or 4 cysteine residues so solitioned

CC that the expressed peptide contains 2 or 4 cysteine residues so conter some degree of contommational rigidity to the peptides. The TSARs

CC cc compans, comprising a TSAR binding domain can be used in vivo to

CC cliver a chemically or biologically active moiety, eg. metal ion,

CC cell. They can also replace the function of macromolecules, eg.

CC call. They can also replace the function of macromolecules, eg.

CC complex methods of hybridoma famila dermation or in vivo antibody

CC activity allowing direct and applid dermation or in vivo antibody

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CC activity allowing direct and applid dermation or in vivo antibody
                                                                                                                                                          151 GCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGACCCGGCGCGTTTCCGCGCGCTGGTGGC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss. Synthetic.
     cobbbggbcbbtttgccbggctggttgcbcgbbctgbttgggttccgbggtgttbgtggb
                                                   CTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTC-GTGCGGCGCCTGGG
                                                                                                         gbtgtttgggggbgbggtctgbgtccbccggggbggbcgttbtccbtttcgbbgctbggcgg
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/*tag= a
//tote= "this sequence represents '2'; Z
sequence of 6, 9 or 12 nucleotides (see
                                                                                                                                                                                                                193 tbbbgccctbctbtctgtbcbcbcccccctctgcbgcb 231
                                                                                                                                                                                                                                        211 CCAGTGCCTGGTGTGCGTGCCCTGGGACGCACGCCCCC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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က
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Q70465 standard; DNA; 114 BP.
Q70465;
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31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWlkes DM, Kay BK;
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A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the substance P receptor, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchtits and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense on, its liberation upon antisense degradation is prevented, thereby preventing adenosine induced broncheconstriction in patients with hyper-reactive airways.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2082 AGGAGGCCGGGCGCCCGCCCGCTGTAGTTGAGCACGCTGAACAGTGCCTTCACCCTC 2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 aaawyccyrrsvkydccynachhddhyvybbbvynvhnhnncncccbnnhvchnvhbnnh 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 aggnyccccgggywccgagcycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsd 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 cobobtobetbecbegttgeecbecbebgbggtcbecbcbbtgbeegtgtbggebgetge 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
                                                                                                                                                                                                                                                                                                                                                                     108 Others;
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Substance P receptor antisense oligonucleotide.
Asthma: airway epithelium; adenosine free; cystic fibrosis; chronic obstructive pulmonary disease; bronchitis; ss.
W09640162-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58; Mismatches 59; Indels
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51; Mismatches 83; Indels
misincorporation, completion of molecules and screening.
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                                                                                                                                                                                                                                                                                                                                                                     11 T;
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Pred. No. 3.20e-08;
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T76445 standard; DNA; 264 BP
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Best Local Similarity 18.8%;
Matches 27; Conservative
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06-JUN-1996; U09306.
07-JUN-1995; US-474497.
(UYEC-) UNIV EAST CARCLINA.
Metzger WJ, Nyce JW;
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Local Similarity 37.9%;
hes 83; Conservative
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                     Disclosure; p; English
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                                                                         Gaps
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                                                 Pred. No. 1.23e-06;
                                  Score 38; DB 12;
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Query Match

Matches

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33

subject

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US-08-912-951-1.rng

070468;

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Generic DNA sequence to generate a random TSAR peptide library.
TSAR; totally synthetic affinity reagent; synthetic; binding domain;
effector domain; concatenated heterofunctional protein; linker;
direct; rapid; detection; screening; treatment; generic; ss.
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/note= "encoded by Z (see comments)"
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Q70467 standard; DNA; 114 BP.
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(UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, KAY BK;
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Best Local Similarity 9.8%;
Matches 11; Conservative
                                        (first entry)
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standard; DNA; 114
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US-176500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terein would be a recombinant vector library expressing fusion proteins acceming a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by screening a bending domain and an effector domain bisclosure; Page 35; 255pp; English.

Comprising a binding domain and an effector domain bisclosure; Page 35; 255pp; English.

Comprising a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reasperts) peptides. This generic formula can also be represented as follows: X(NNB)11(TGC)(NNB)52(NNB)7(TGC)(NNB)10V. X and Y are flanking restriction sites (X is not the same as Y) that are cont specific peptides generated by these generic sequences are shown in K85151-54. TSARs are concatenated heterofunctional proteins or peptides, other specific peptides generated by these generic sequences are shown in K85151-54. TSARs are concatenated heterofunctional proteins or peptides, of affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of frainty for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker of frainty for be used for variant residues. These residues conformations comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, addition and also replace the function of macromolecules, eg. comprising a TSAR binding domain cancentre the recomplex methods of hybridomal antibodies and therefore circumvent the need for complex methods of hybridomal antibodies and therefore circumvent the need for complex methods of hybridomal antibodies and therefore directing process.

Callowing direct and rapid detection in a screening process.
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                                                            2539 CCAGGGGATCCCGCAGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGC 2590
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                 200 GCGCTGGTGGCCCAGTGCCTGGTGCGTGCCTGGGACGCACGGCCGCCC 251
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Pred. No. 1.23e-06;
34; Mismatches 73; Indels
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sequence of 6, 9 or 12 nucleotides (see
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWIKES DM, KAY BK;
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4.58;
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Q70468 standard; DNA; 114
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P-PSDB; R65154.
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Tidentifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins of comprising a binding domain and an effector domain bisclosure; Page 36: 255pp; English.

Disclosure; Page 36: 255pp; English.

Offinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)4CAC)(NNB)8Z(NNB)6(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8Z(NNB)7X And Y are flanking restriction sites (x is not the same of other generic sequences (07041-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated by this and other generic sequences (07041-73) have invariant histidine residues incorporated into variant sequences. TSARs are concatenated by this and carginos - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They can comprise a linker peptide between the 2 domains. The TSARs or comprising a TSAR binding domain can be used in vivo to deliver a chemically to biologically active mobiety, eg metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the composition of peptides and therefore circumvent the need composition of the function of macromolecules, eg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generic DNA sequence to generate a random TSAR petide library. TSAR: totally synthetic affinity reagent; synthetic; binding domain; effector domain; concateneated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; generic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bnnbnnbnnbcacnnbnnbnnbnnbcacnnbnnbnnbnnbnnbnnbnnbnnbnnnnnn 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening proce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಹ
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/note= "this sequence represents 'Z'; Z can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 12; Length 114
Pred. No. 1.33e-05;
30; Mismatches 71; Indels
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14

RESULT

Matches

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Tightlifying proteins or peptide(s) which bind a ligand - by acreening a recombinant vector library expressing fusion proteins by screening a recombinant vector library expressing fusion proteins by acreening a recombinant vector library expressing fusion proteins. By acreening a recomprision a blinding domain and an effector domain bisclosure; Page 35; 255pp; English.

CC 700467 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affility Reagents) peptides. This generic formula can also be represented as follows: X(NNB)16(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(NNB)12(TGC)(TRA) are concatenated heterofunctional proteins or peptides.

CC and X are flanking restrictions regions a binding domain with the septides generated betterofunctional proteins or peptide portion that is chart the arbitrary and as second effector peptide portion that is chart the axpressed peptide contains 2 or 4 crysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confers some degree of conformational rigidity to the peptides. The TSARs or compass, comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active molety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the conformation or mishods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in ascormanced and ascormanced ascormanced and ascormanced and ascormanced and ascor
sequence of 6, 9 or 12 nucleotides (see comments)"
                                                                                                                                                                                                                                                             (UYNC-) UNIV NORTH CAROLINA.
Fowlkes DM, Kay BK;
WPI; 94-279739/34.
P-PSDB; R65153.
                                                                                                                                                                      01-FEB-1993; US-013416.
30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
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0; Gaps Score 36; DB 12; Length 114; Pred. No. 1.33e-05; 34; Mismatches 74; Indels Query Match 0.9%; Best Local Similarity 3.6%; Matches 4; Conservative Query Match

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88 CICCCIGCIGCGCAGCCACTACCGCGAGGIGCIGCCGCIGGCCACGIICGIGCGGCGCCI 147

ద ò 148 GGGGCCCCAGGCTGGGGGGCTGGGGGGGGGGCCCGGCGCGCTTTCCGC 199

Search completed: Mon Aug 3 16:47:21 1998 Job time: 1666 secs.

<u> </u> ;//

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

n.a. - n.a. database search, using Smith-Waterman algorithm MPsrch_nn

MasPar time 4562.35 Seconds 1232.517 Million cell updates/sec Mon Aug 3 10:56:05 1998; bular output not generated. .. 0

>US-08-912-951-1 (1-4015) from USO8912951.seq 4015 Description: Perfect Score: N.A. Sequence: Comp: Title:

TABLE default Gap 6 Scoring table:

Dbase 0; Query 0 STD Nmatch

Searched:

×

1832099 segs, 700269816 bases

Minimum Match 0% Listing first 45 summaries Post-processing:

embl-est55 Database:

1:em_est10 2:em_est11 genbank-est107 Database:

3:9b_est1 4:9b_est10 5:9b_est11 6:9b_est12 7:9b_est13 8:9b_est14 9:9b_est15 10:9b_est16 11:9b_est17 12:9b_est18 13:9b_est19 14:9b_est2 15:9b_est20 16:9b_est2 17:9b_est2 18:9b_est2 18:9b_est2 17:9b_est2 18:9b_est2 19:9b_est3 19:9b_est3 20:9b_est6 23:9b_est7 24:9b_est8 25:9b_est9 26:9b_est9 26:9b_est8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Variance 2.606; scale 4.689 Mean 12.222; istics:

SUMMARIES

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Pred. No.	0.00e+00	0.00e+00	0.00e+00	0.00e+00	2.68e-65	5.79e-62	5.26e-57	2.34e-39	6.37e-41	2.86e-13	1.04e-10	2.86e-13	2.86e-13
Description	zt08902.rl NCI CGAP GC		ny02e05.sl NCI_CGAP_GC	EST182469 Jurkat T-cel	97SN1784 Rice Immature	97SN1787 Rice Immature	97SN1787 Rice Immature	97SN1784 Rice Immature	EST12462 Uterus tumor	mul3h09.rl Soares 2NbM	Homo sapiens ntcon6 co	Homo sapiens ntcon2 co	Homo sapiens ntcon2 co
ID	AA281296	AA811084	AA748707	AA311750	AA754458	AA754459	AA754459	AA754458	AA299878	AA200728	AF034177	AF034173	AF034173
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& Query Match	9.6	7.8	7.1	6.2	1.7	1.6	1.5	1.3	1.3	9.0	0.8	0.8	0.8
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3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified priz3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

About taxef="taxon:9606"

Alone="IMAGE:712562"

Alone="IM
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Tel: (301) 496-1550
Email: Robert_Strausberg@ih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Elmates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 340)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
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Pred. No. 0.00e+00;
0; Mismatches 2;
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l Similarity 99.5%;
387; Conservative
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Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 AATTTGACCCACAGG-ACCCCCATCCAGGTGCAGGGTCCTCGCCTGTGTACAGGGCACAC 130
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 315)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Pred. No. 0.00e+00;
0; Mismatches 1;
                                                                                   Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 331.
Location/Qualifiers
                                  www-bio.llnl.gov/bbrp/image/image.html
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                                                                      Std
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Best Local Similarity 99.1%;
Matches 328; Conservative
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AUTHORS
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                                                                                                                         FEATURES
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19-APR-1997

JOURNAL

COMMENT

TITLE

ATURES

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Locates I. C. 409]

Moders M. C. Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.J., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.F., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Colleman, T.A., Collins, E.J.,
Dumke, D., Feng, D.-F., Ferriet, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melson, P., Kim, A.K.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Praser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
19712 Email: arkerlav@tigr.org
19712 Email: arkerlav@tigr.org
19712 Additional sequence and expression
19712 Additional Sequence and expression
19712 Additional Sequence Check the Tigr Human Gene
                                                                                                                                                                                                                                   Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
xhor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GGACCCTGGTCCGAGGTGTCCCTGAGTATGCTGCGTGTGAACTTGCGGAAGACAGTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGAACTICCCTGTAGAAGACGAGGCCCTGGGTGCCACGGCTTTINTTCAGATGCCGGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2709 GGACCCTGGTCCGAGGTGTCCCTGAGTATGCTGCGTGGTGAACTTGCGGAAGACAGTGG
                                AA311750 409 bp mRNA EST 19-APR-1:
EST182469 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="ATCC (inhost):158964"
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<1. .>409
a 120 c 133 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 248; DB 4; Le
Pred. No. 0.00e+00;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.28;
                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 409)
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les 248; Conservative
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                                                                                          sequence.
AA311750
91964077
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                                                             DEFINITION
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Matches
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     RESULT
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3955 AATTTGACCCACAGGGACCCCCATCCAGGTGCAGGGTCCTCGCCTGTGTACAGGGCACAC 3896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3895 CITIGETCACTCCAAATICCCAGAGCTCCCAGGGTCCTTCTCAGGGTCTCCACCTGGATG 3836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3835 GTGGGGGT-GGAAGGCAAAGGAGGGCGAGGGGTGAATGCGCGAATCTGGGGAT 3777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3776 GGACTATTCCTATGTGGGGAGTGGAAGCCGGGCTCCTGGTGAAGAAAAGCTGGCCCTGGG 3717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTTGACCCACAGGGACCCCCATCCAGGTGCAGGGTCCTCGCCTGTGTACAGGGCACAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTTGGTCACTCCAAATTCCCAGAGCTCCAGGGTCCTTCTCAGGGTCTCCACCTGGATG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Bento Soares and M. Fatima Bonaldo." /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GGACTATTCCTATGTGGGGGGTGGAAGCCGGGCTCCTGGTGAGGAAAAGCTGGCCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGGCCCCGGCCCCCAAACCACGCCACGCCGAGGGGTGAACAATGGCGAATCTGGGGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 285; DB 15; Length 315; Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1270592"
/clone_lib="NGI_CGAP_GCB1"
/tissue_type="germinal center B cell"
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95 c 87 g 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 1226 Std Error: 0.00
Seq prime: -40m13 fwd. Er from Amersham
High quality sequence stop: 281.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 96.2%;
Matches 302; Conservative
                                                                                                                                         Tel: (301) 496-1550
Email: Robert_Straus
                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3716 GTGGAGCCGAGCGC 3703
                                Tumor Gene Index
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BASE COUNT ORIGIN

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Gaps

Indels

Length 409;

181

121

61

윱 გ 셤 å 유 გ 셤 S 유

5 others

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97SN1787 Rice Immature Seed Lambda ZAPII CDNA Library Oryza sativa cDNA clone 97SN1787, mRNA sequence.
AA754459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
/cultivar="Milyang23"
/note="Vector: PBluescript SK(+); Site_1: EcoRI; Site_2:
Xhoi: Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                        Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Bubryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 252)
Nahm,B.H., Kim,M.Y., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,M.T., Kim,M.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="97SN1787"
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/dev_stage="5 days after pollination"
/lab_host="E. coll SOLR"
/lab_host="E. 12 g 35 t 179 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS AA754459 252 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1787 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kynggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 WBVBNTKVDVGNHTRCSRWRBVTRMAHYHDYTNCBBYNNNDYHMWHBBMYBBTGCMTCTM 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 WCWBHYNTKCTASGWHTSTNYDVKSSTNTWGVTBSYDKSMHGYWCSBBVKYHTKVSTTRA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ISYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWSTMTW-GTVNWBNVSGDWHY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          826 GGCCCAGGACCCCTGCCCAACGGGCGTCCGCTCCGGCTCAGGGGCAGCGCCACGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.6%; Score 65; DB 13; Length 252; Best Local Similarity 12.4%; Pred. No. 5.79e-62; Matches 27; Conservative 114; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGC--AGGCCCAGGGGACCCCGGCCTCCCTGACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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    |::: :|:|:
1226 GCCGCATTTG 1217
                                                                                                                                                                                                                                                                                    Oryza sativa
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                                                                                                                                           DEFINITION
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                                                                                                                                                                                          ACCESSION
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                                                                                                                                                                                                                                                                        97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa cDNA clone 97SN1784, mRNA sequence.
4A754458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-Voctor: pBluescript SK(+); Site_1: EcoRI; Site_2:
Xhol; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
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/clone="97SNIXR4"
/clone="type="Immature Seed"
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/lab_host="Ecoli SOLR"
a 16 c 21 g 34 t 169 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongjl
University, Yongin, Rorea. 449-728 bhnahm@bioserver.myongjl.ac.kr
Seq primer: M13 Reverse Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.S.
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                                                                    2829 ACGCCCTATTCCCCTGGTGCGGCCTGCTGCTGGTACCCGGACCCTGGAGGTGCAGAGGC 2888
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2769 TGAACTICCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCC
                                              181 ACGCCNTATTCCCCTGGTGCGCCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGGG
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Larity 14.7%; Pred. No. 2.68e-65;
Conservative 101; Mismatches 58
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                                                                                                                                         241 ACTACTCCAG 250
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Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; oryza.
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/dev_stage="5 days after pollination"
/lab_lost="E. coli SOLR"
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National Inst. of Agri. Sci. and Tech, RDA
Wational Inst. of Agri. Sci. and Tech, RDA
Wational Inst. of Agri. Sci. and Tech, RDA
Tel. 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bloserver.myongji.ac.kr
Location/Qualifiers
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Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R, Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.
Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
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/cultivar="Milyang23"
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                            ACCESSION
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KEYWORDS
                                                                                                          KEYWORDS
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ORIGIN

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1 (bases 1 to 303)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock, K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar-"Milyang23"
/note-"Vector: paluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4330"
/clone="97SN1784"
/clone=11b="Raice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
a 16 c 21 g 34 t 169 others
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                  Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Fax: 82 391 290 0307
Faxi. 82 391 290 0307
Small: myeun(%sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ~
                                                      1 (bases 1 to 247)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA299878 303 bp mRNA EST 18-APR-1997
EST12462 Uterus tumor I Homo sapiens CDNA 5' end, mRNA sequence.
AA299878
                                                                                                                                                                                                        Large-scale Sequencing Analysis of ESTs from Rice Immature Seed Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1732 ITTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAG 1791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 YGTBYYSWNYDINTGGTGVGKTTVNVHSGWNNRCSNSVVYVWBTAYCDYBHYBDRANHVD 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 DTRCINDRGYCN-YTASDNGTSATKRVTGYDKTDSDCGGGCWRKVTYGSSBYBRCGVNVM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 BAMMNKHIHMMIBBWCCVRRVGITINNGKHNGRITIWNDCSDNAHCRYIVBWYYARSKYG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 VRTTSMWTDKSTKMBSMDMSRRSRVHYGRWMBNKKRGMS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.3%; Score 51; DB 13;
Best Local Similarity 10.5%; Pred. No. 2.34e-39;
Matches 23; Conservative 108; Mismatches 86
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DEFINITION
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Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marnaros, S.M., Merrick, J.M.,
Moreno-Pealaquees, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Lu, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dlumke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, C.B., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillion, P.J., Pannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleoides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 375)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TigR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA200728 375 bp mRNA EST 19-FEB-1997 mul3h09.rl Soares 2NbWT Mus musculus cDNA clone 639329 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGACACGGCCTCCCTCTGCTACTCCTGAAAGCCAAGAACGCAGGTATGT 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 303;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 4; I
Pred. No. 6.37e-41;
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WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .303
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.
The WashU-HHMI Mouse EST Project
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Best Local Similarity 98.1%;
Matches 53; Conservative
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C
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AA200728
g1795738
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LOCUS
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JOURNAL
COMMENT
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SOURCE
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Central Deuts of the Magoussis, J.

Lospital, 7th floor, Guy's Tower, London SE1 9RT, UK

Location/Qualifiers

Central Central
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Homo sapiens ntcon6 contig mRNA, partial sequence, mRNA sequence.
AF034177
92707739
                                                                                                                                                                                              This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:391321
Seq primer: -28MJ3 rev2 from Amersham
High quality sequence stop: 361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2436 AGAGCICCICCCIGAAIGAGGCCAGCAGIGGCCICITCGACGICTICCACGITCAIGI 2495
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Bukaryotae, Matazoa, Chordata, Vertebrata; Mammalia; Butheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
Tripodis,N. and Ragoussis,J.
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fars: 314 286 1810
Email: mouseest@watson.wustl.edu
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Pred. No. 2.86e-13;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 0.8%;
Local Similarity 75.4%;
nes 49; Conservative
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DEFINITION
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ORIGIN
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2 (bases 1 to 2275)
Tripodis, n and Ragoussis, J.
Submitted (13-NOV-1997) Division of Medical and Molecular Genetics, Guy's Hospital, 7th floor, Guy's Tower, London SEI 9RT, UK
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                                                                                                                                                                                                                                                                                      AF034173 2275 bp mRNA EST 22-DEC-1997 AF034173 22-DEC-1997 MRNA, partial sequence, mRNA sequence. 92707735
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Memo sapiens ntcon2 contig mRNA, partial sequence, mRNA sequence.
AF034173
92707735
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/chromosome="6"
/map="6p21.3"
/clone="ntcon6 contig"
/tissue_retal brain; fetal liver; adult muscle"
/note="similar to CutA"
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarnhin; Hominidae; Homo.

1 (bases 1 to 2275)

Tripodis,N. and Ragoussis,J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
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                                                                                                                             Length 660;
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                                                                                 55 others
                                                                                                                             Score 31; DB 12; Length 660
Pred. No. 1.04e-10;
31; Mismatches 7; Indels
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Pred. No. 2.86e-13;
47; Mismatches 25; Indels
                                                                                                                                                                                                            336 AGAACGTGGCCTTCGCTTCGCTCTCGCTGGACGGGCCCGCG 380
                                                                                                                                                                                            384 WSSRCCYRSYGMYHYYYCYYKKCDMSCTTSKSRWYKSKRSWCDCD 428
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/clone="ntcon2 contig"
/tissue_type="liver; brain"
/dev_stage="fetus"
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/chromosome="6"
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Best Local Similarity 13.3%;
Matches 11; Conservative
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Best Local Similarity 15.6%;
Matches 7; Conservative
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Unpublished

2 (bases 1 to 2275)

Tripodis,u. and Ragoussis,J.

Direct Submission

Submitted (13-NOV-1997) Division of Medical and Molecular Genetics,

Guy's Hospital, 7th floor, Guy's Tower, London SE1 9RT, UK

Location/Qualifiers
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21;
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2692 GIGGGTGAGGTGACCAACAAGAAATCATCCACCAAACGCAGGAGGAGCCCGTC 2633
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Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
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CIT-HSP-2288C3.TF CIT-HSP Homo sapiens genomic clone 2288C3,
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1542 YKSWSRWYWYTTYTYWY - CWCCTSMKSASCAMMRWMGYMGSRSSRSYWGYWGSMS 1595
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/clone="ntcon2 contig"
/tissue_type="liver; brain"
/dev_stage="fetus"
/note="similar to Br140"
a 619 c 470 g 599 t
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/db_xref="taxon:9606"
/chromosome="6"
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1. .317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="6p21.3"
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Best Local Similarity 13.0%;
Matches 15; Conservative
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Search completed: Mon Aug
Job time : 8704 secs.
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Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

Funates; Catarrhini; Hominidae; Homo.

(bases 1 to 560)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,

Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Febr. 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
Location/Qualifiers
1. Se0
/organism="Homo sapiens"
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/lab_host="SOLR cells (kanamycin resistant)"
118 c 134 g 135 t
                                                                                                                                                           Length 317;
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                                                                                                                                                       Score 27; DB 26; Length 317
Pred. No. 6.67e-06;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                      231 CCTTTCCCCAGGTGTCCTGTCTGAAGGAGATGGGGGC 267
                                                                                                   75 t
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/clone_llb="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
a 92 c 91 g
/db_xref="taxon:9606"
                                                                                                                                                       Query Match 0.7%;
Best Local Similarity 86.5%;
Matches 32; Conservative
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